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<!--StartFragment-->RESULT 2
ADC00348
ID   ADC00348 standard; protein; 441 AA.                    Appendix    A
XX
AC   ADC00348;
XX
DT   15-JUN-2007  (revised)
DT   04-DEC-2003  (first entry)
XX
DE   Enterohaemorragic E. coli 0157:H7-specific protein SEQ ID NO: 393.
XX
KW   enterohaemorragic; anti-bacterial; BOND_PC; hypothetical protein;
KW   hypothetical protein ECs1812 [Escherichia coli O157:H7];
KW   hypothetical protein ECs1812 [Escherichia coli O157:H7 str. Sakai];
KW   unknown protein encoded by cryptic prophage CP-933P;
KW   hypothetical protein [Escherichia coli O157:H7 str. Sakai].
XX
OS   Escherichia coli; 0157:H7.
XX
PN   JP2002355074-A.
XX
PD   10-DEC-2002.
XX
PF   24-JAN-2002; 2002JP-00015959.
XX
PR   24-JAN-2001; 2001JP-00112010.
XX
PA   (UYTS-) UNIV TSUKUBA.
XX
DR   WPI; 2003-451640/43.
DR   PC:NCBI; gi13259568.
XX
PT   Enterohemorragic Escherichia coli O157:H7-specific nucleic acid molecule
PT   and a polypeptide and its use, a polypeptide, a vector and a host cell.
XX
PS   Claim 3; SEQ ID NO 393; 2067pp; Japanese.
XX
CC   The invention relates to a novel enterohaemorragic Escherichia coli
CC   O157:H7-specific nucleic acid molecule. A polynucleotide of the invention
CC   has anti-bacterial activity. The polypeptide can be used in detection
CC   and/or treatment of 0157:H7 infection. The nucleotide sequence of the
CC   genome of Enterohaemorragic E coli 0157:H7 was determined. The present
CC   sequence represents an E. coli 0157:H7-specific polypeptide of the
CC   invention.
CC
CC   Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 441 AA;

  Query Match                84.1%;   Score 1943.5;  DB 6;   Length 441;
  Best Local Similarity    81.0%;   Pred. No. 5.8e-175;
  Matches  359;  Conservative   32;  Mismatches   37;  Indels   15;  Gaps    3;

Qy        1 MNIQPNIHSGITTQNNQQHHHAEQVPVSSSIPRSDLPPNCEAGFVVHIPEDIQQHVPECG 60
            ||||| | ||||:||| |||  ||:| |: ||:|:|| |:|||||:||:||||| ||||
Db        1 MNIQPTIQSGITSQNN-QHHQTEQIP-STQIPQSELPLGCQAGFVVNIPDDIQQHAPECG 58

Qy       61 ETTALLSLIKDEGLLSGLDKYLAPHLEEGSLGKKALDTFGLFNVTQMALEIPSSVPGISG 120
            |||||||||||:||||||||:|:||||||||:||| || ||||||||||||||||| ||||
Db       59 ETTALLSLIKDKGLLSGLDEYIAPHLEEGSIGKKTLDMFGLFNVTQMALEIPSSVSGISG 118

Qy      121 KYGVQMNIVKPDIHPTTGNYFLQLFPLHDEIGFNFKDLPGPLKNALTNSSI--------- 171
            |||||:|||||||||:||||||:||||||||||||||||||||||||||:||:|
Db      119 KYGVQLNIVKPDIHPTSGNYFLQIFPLHDEIGFNFKDLPGPLKNALSNSNISTTAVSTIA 178

Qy      172 ----SATASTVAPTPNDPMPWFGLTAQVVRNHGVELPIVKTENGWKLVGETPLTPDGPKA 227
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                   ||| |||    | ||:||||||||||||||||||||||||||||||||||||||||
Db        179 STGTSATTSTVTTEPKDPIPWFGLTAQVVRNHGVELPIVKTENGWKLVGETPLTPDGPKA 238

Qy        228 NYTEEWVIRPGEADFKYGTSPLQATLGLEFGAHFKWDLDNPNTKYAILTNAAANAIGAAG 287
              ||||||||||||||||| ||||||||||||||||||||||||||:|||||||:|| |
Db        239 NYTEEWVIRPGEADFKYGASPLQATLGLEFGAHFKWDLDNPNTKYAVLTNAAANALGALG 298

Qy        288 GFAVSKVPGIDPMLSPHVGAMLGQAAGHAVQCNTPGLKPDTILWWAGATFGAADLNKAEF 347
              |||||:    |||||||:|||:||||||:| ||||||||||||||| |||||||||||
Db        299 GFAVSRFASTDPMLSPHIGAMVGQAAGHAIQYNTPGLKPDTILWWAGATLGAADLNKAEF 358

Qy        348 DKVRFTDYPRIWFHAREGALFPNKQDIARVTGADIKAMEEGVPVGHQHPKPEDVVIDIEG 407
              :  |||||||||:||||||:|||| ||     |||||:|||||:||| :|| ||||||||||
Db        359 EVARFTDYPRIWWHAREGAIFPNKADIEHATGADIRAMEEGIPVGQRHPNPEDVVIDIES 418

Qy        408 GNSPHHNPSNYVDTFEIIQETRV 430
              |||||||:|| |:|||||||||
Db        419 NGLPHHNPSNHVDIFDIIQETRV 441
<!--EndFragment-->
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